

SEQUENCE LISTING

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<130> 3206-169/PAR

<140> PCT/CA99/00375

<141> 1999-04-27

<150> 2,230,201

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<170> PatentIn Ver. 2.0

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gaa cga aaa gct gag gca aaa caa agt gag aca gcc agt gct ttg gtg Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val 705 710 715 720	2160
aat tac aga gca ctg tac cct ttt gaa gca aga aac cat gat gag atg Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met 725 730 735	2208
agt ttt agt tct ggg gat ata att cag gtt gat gaa aaa act gta gga Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly 740 745 750	2256
gag cct ggt tgg ctt tat ggt agt ttt cag gga aag ttt ggc tgg ttc Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe 755 760 765	2304
ccc tgc aac tat gta gaa aaa gtg ctg tca agt gaa aaa gct ctg tct Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser 770 775 780	2352
cct aag aag gcc tta ctt cct cct aca gtg tct ctc tct gct acc tca Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser 785 790 795 800	2400
act tct tcc cag cca cca gca tca gtg act gat tat cac aat gta tcc Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser 805 810 815	2448
ttc tca aac ctt act gtt aat aca aca tgg cag cag aag tca gct ttt Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe 820 825 830	2496
acc cgc act gtg tcc cct gga tct gtg tcc ccc att cac gga cag ggg Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly 835 840 845	2544
cag gct gta gaa aac ctg aaa gcc cag gcc ctt tgt tcc tgg acg gca Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala 850 855 860	2592
aag aag gag aac cac ctg aac ttc tca aag cac gac gtc atc act gtc Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val 865 870 875 880	2640

ctg gag cag cag gaa aac tgg tgg ttt ggg gag gtg cac gga gga aga	2688
Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg	
885 890 895	
gga tgg ttc ccc aag tct tat gtc aag ctc att cct ggg aat gaa gta	2736
Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val	
900 905 910	
cag cga gga gag cca gaa gct ttg tat gca gct gtg act aag aaa cct	2784
Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro	
915 920 925	
acc tcc aca gcc tat cca gtt acc tcc aca gcc tat cca gtt gga gaa	2832
Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu	
930 935 940	
gac tac att gca ctt tat tca tac tca agt gta gag ccc ggg gat ttg	2880
Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu	
945 950 955 960	
act ttc act gaa ggt gaa gaa att cta gtg acc cag aaa gat gga gag	2928
Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu	
965 970 975	
tgg tgg aca gga agt att gga gag aga act gga atc ttc ccg tcc aac	2976
Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn	
980 985 990	
tac gtc aga cca aag gat caa gag aat ttt ggg aat gct agc aaa tct	3024
Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser	
995 1000 1005	
gga gca tca aac aaa aaa ccc gag atc gct caa gta act tca gca tat	3072
Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr	
1010 1015 1020	
gct gct tca ggg act gag cag ctc agc ctt gcg cca gga cag tta ata	3120
Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile	
1025 1030 1035 1040	
tta atc tta aag aaa aac aca agc ggg tgg tgg caa gga gag cta cag	3168
Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln	
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gcc aga ggg aag aaa cga cag aag gga tgg ttt cct gcc agc cat gta	3216
Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro Ala Ser His Val	
1060 1065 1070	
aag ctg cta ggt cca agc agt gaa aga acc atg cct act ttt cac gct	3264
Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met Pro Thr Phe His Ala	
1075 1080 1085	
gta tgt caa gtg att gct atg tat gac tac atg gcg aat aac gaa gat	3312
Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Met Ala Asn Asn Glu Asp	
1090 1095 1100	
gag ctc aat ttc tcc aaa gga cag ctg att aat gtt atg aac aaa gat	3360
Glu Leu Asn Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys Asp	
1105 1110 1115 1120	

gac cct gac tgg tgg caa gga gaa acc aat ggt ctg act ggt ctc ttt 3408  
 Asp Pro Asp Trp Trp Gln Gly Glu Thr Asn Gly Leu Thr Gly Leu Phe  
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cct tca aac tat gtt aag atg aca aca gac tca gat cca agt caa cag 3456  
 Pro Ser Asn Tyr Val Lys Met Thr Thr Asp Ser Asp Pro Ser Gln Gln  
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tgg tgt gct gac ctc caa gcc ctg gac aca atg cag cct acg gag agg 3504  
 Trp Cys Ala Asp Leu Gln Ala Leu Asp Thr Met Gln Pro Thr Glu Arg  
                   1155                  1160                  1165

aag cga cag ggc tac att cac gag ctc att cag aca gag gag cgg tac 3552  
 Lys Arg Gln Gly Tyr Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr  
                   1170                  1175                  1180

atg gac gac ctg caa ctt ttt gaa caa aaa act ctc ctt tga 3594  
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 <212> PRT  
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                   20                  25                  30

Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe  
                   35                  40                  45

Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu  
                   50                  55                  60

Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile  
                   65                  70                  75                  80

Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val  
                   85                  90                  95

Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile  
                   100                  105                  110

Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln  
                   115                  120                  125

Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr  
                   130                  135                  140

Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro  
                   145                  150                  155                  160

Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln  
                   165                  170                  175

Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser  
 180 185 190  
 Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala  
 195 200 205  
 Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala  
 210 215 220  
 Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val  
 225 230 235 240  
 Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp  
 245 250 255  
 Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu  
 260 265 270  
 Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu  
 275 280 285  
 Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu  
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 Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu  
 305 310 315 320  
 Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln  
 325 330 335  
 Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu  
 340 345 350  
 Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys  
 355 360 365  
 Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val  
 370 375 380  
 Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu  
 385 390 395 400  
 Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp  
 405 410 415  
 Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu  
 420 425 430  
 Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu  
 435 440 445  
 Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg  
 450 455 460  
 Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp  
 465 470 475 480  
 Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu  
 485 490 495

Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val  
 500 505 510  
 Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys  
 515 520 525  
 Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu  
 530 535 540  
 Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu  
 545 550 555 560  
 Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser  
 565 570 575  
 Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys  
 580 585 590  
 Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser  
 595 600 605  
 Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg  
 610 615 620  
 Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile  
 625 630 635 640  
 Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile  
 645 650 655  
 Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly  
 660 665 670  
 Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Lys  
 675 680 685  
 Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu  
 690 695 700  
 Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val  
 705 710 715 720  
 Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met  
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 Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly  
 740 745 750  
 Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe  
 755 760 765  
 Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser  
 770 775 780  
 Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser  
 785 790 795 800  
 Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser  
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Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe  
 820 825 830  
 Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly  
 835 840 845  
 Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala  
 850 855 860  
 Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val  
 865 870 875 880  
 Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg  
 885 890 895  
 Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val  
 900 905 910  
 Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro  
 915 920 925  
 Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu  
 930 935 940  
 Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu  
 945 950 955 960  
 Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu  
 965 970 975  
 Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn  
 980 985 990  
 Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser  
 995 1000 1005  
 Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr  
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 Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile  
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 1045 1050 1055  
 Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro Ala Ser His Val  
 1060 1065 1070  
 Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met Pro Thr Phe His Ala  
 1075 1080 1085  
 Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Met Ala Asn Asn Glu Asp  
 1090 1095 1100  
 Glu Leu Asn Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys Asp  
 105 1110 1115 1120  
 Asp Pro Asp Trp Trp Gln Gly Glu Thr Asn Gly Leu Thr Gly Leu Phe  
 1125 1130 1135



Pro Ser Asn Tyr Val Lys Met Thr Thr Asp Ser Asp Pro Ser Gln Gln  
1140 1145 1150

Trp Cys Ala Asp Leu Gln Ala Leu Asp Thr Met Gln Pro Thr Glu Arg  
1155 1160 1165

Lys Arg Gln Gly Tyr Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr  
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<212> DNA  
<213> Mus musculus

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agaagaaacg ggaaaaggct taccaagccc gttctcaaaa gacttcagggt attgggcgtc 180  
tgatggtgca tgtcattgaa gctacagaat taaaagcctg caaaccaaac gggaaaagta 240  
atccatactg tgaagtcagc atgggctccc aaagctatac caccaggacc ctgcaggaca 300  
cactaaaccc caagtgaac ttcaactgcc agttcttcat caaggatctt taccaggacg 360  
ttctgtgtct cactatgttt gagagagacc agttttctcc agatgacttc ttgggtcgta 420  
ctgaagttcc agtggcaaaa atccgaacag aacaggaaag caaaggcccc accaccgcc 480  
gactactact gcacgaagtc cccactggag aagtctgggt ccgctttgac ctgcaacttt 540  
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aggctgggtc taaagacaga ttttgccttc ccaggacaga ggagcatcac atggcttcat 660  
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Glu Gln Tyr Ile Asp Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr Gln  
35 40 45

Ala Arg Ser Gln Lys Thr Ser Gly Ile Gly Arg Leu Met Val His Val  
 50 55 60  
 Ile Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn Gly Lys Ser Asn  
 65 70 75 80  
 Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser Tyr Thr Thr Arg Thr  
 85 90 95  
 Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn Phe Asn Cys Gln Phe Phe  
 100 105 110  
 Ile Lys Asp Leu Tyr Gln Asp Val Leu Cys Leu Thr Met Phe Asp Arg  
 115 120 125  
 Asp Gln Phe Ser Pro Asp Asp Phe Leu Gly Arg Thr Glu Val Pro Val  
 130 135 140  
 Ala Lys Ile Arg Thr Glu Gln Glu Ser Lys Gly Pro Thr Thr Arg Arg  
 145 150 155 160  
 Leu Leu Leu His Glu Val Pro Thr Gly Glu Val Trp Val Arg Phe Asp  
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 Leu Gln Leu Phe Glu Gln Lys Thr Leu Leu  
 180 185

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 ttttaagccca gccagaaagg cttttcagga ggaaccaagt ccttcatgga ctttggcagc 180  
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 gggcgtggcc tggggaagaa cgcacagggg atcatcaacc ccatcgaagc caaacagaga 300  
 aaaggcaagg gagccgtggg ggcctatggc tcggagagga ccactcagtc tctgcaggac 360  
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 tggaggaaag accccagcgg gagcaagaag aagccaaagt actcttaca gactgtggag 480  
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 acagccggca aggaagccag gatgccgggc ttgactgctg ctgagctgga gcacaacctg 720  
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gagcgggaca tgggtggtcag cctgtcgcat gagctggaga agacggccga gggtcttgc 840  
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gagacactac aggacaagta ttatgaggag taccgcctgg cggaccgcgc agacctcgct 1020  
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<211> 309  
<212> PRT  
<213> Mus musculus

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Gly Leu Gly Lys Asn Ala Gln Gly Ile Ile Asn Pro Ile Glu Ala Lys  
35 40 45  
Gln Arg Lys Gly Lys Gly Ala Val Gly Ala Tyr Gly Ser Glu Arg Thr  
50 55 60  
Thr Gln Ser Leu Gln Asp Phe Pro Val Ala Asp Ser Glu Glu Glu Ala  
65 70 75 80  
Glu Glu Glu Phe Gln Lys Glu Leu Ser Gln Trp Arg Lys Asp Pro Ser  
85 90 95  
Gly Ser Lys Lys Lys Pro Lys Tyr Ser Tyr Lys Thr Val Glu Glu Leu  
100 105 110  
Lys Ala Lys Gly Arg Val Ser Lys Lys Leu Thr Ala Pro Gln Lys Glu  
115 120 125  
Leu Ser Gln Val Lys Val Ile Asp Met Thr Gly Arg Glu Gln Lys Val  
130 135 140  
Tyr Tyr Ser Tyr Ser Gln Ile Ser His Lys His Ser Val Pro Asp Glu  
145 150 155 160  
Gly Val Pro Leu Leu Ala Gln Leu Pro Pro Thr Ala Gly Lys Glu Ala  
165 170 175  
Arg Met Pro Gly Phe Ala Leu Pro Glu Leu Glu His Asn Leu Gln Leu  
180 185 190  
Leu Ile Glu Arg Thr Glu Gln Glu Ile Ile Gln Ser Asp Arg Gln Leu  
195 200 205  
Gln Tyr Glu Arg Asp Met Val Val Ser Leu Ser His Glu Leu Glu Lys  
210 215 220

Thr Ala Glu Val Leu Ala His Glu Glu Arg Val Ile Ser Asn Leu Ser  
 225 230 235 240

Lys Val Leu Ala Leu Val Glu Glu Cys Glu Arg Arg Met Gln Pro His  
 245 250 255

Gly Thr Asp Pro Leu Thr Leu Asp Glu Cys Ala Arg Ile Phe Glu Thr  
 260 265 270

Leu Gln Asp Lys Tyr Tyr Glu Glu Tyr Arg Leu Ala Asp Arg Ala Asp  
 275 280 285

Leu Ala Val Ala Ile Val Tyr Pro Leu Val Lys Asp Tyr Phe Lys Asp  
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Trp His Pro Ser Arg  
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 <212> DNA  
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 <212> DNA  
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 <212> DNA  
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<400> 14

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aggttgtaag tgtcttaaag tccttattat caaatcttga tgaaatcaag aaggaaagag 240  
agagtcttga gaatgacctg aagtcagtga attttgacat gacaagcaag tttttgacag 300  
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Pro Arg Thr Met Pro	Pro Ala Lys Pro	Gln Pro Pro Ala	Arg Pro Pro
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<211> 1738

<212> DNA

<213> Mus musculus

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		210				215					220						
tcc	ctc	tca	ggg	aac	tca	cct	aag	aca	ggg	acc	tca	gag	tgg	gca	gtt	720	
Ser	Leu	Ser	Gly	Asn	Ser	Pro	Lys	Thr	Gly	Thr	Ser	Glu	Trp	Ala	Val		
	225				230					235					240		
cct	cag	cct	tca	aga	tta	aag	tat	cgg	caa	aaa	ttt	aat	agt	cta	gac	768	



Pro	Gln	Pro	Ser	Arg	Leu	Lys	Tyr	Arg	Gln	Lys	Phe	Asn	Ser	Leu	Asp	
				245					250					255		
aaa	ggc	atg	agc	gga	tac	ctc	tca	ggg	ttt	caa	gct	aga	aat	gcc	ctt	816
Lys	Gly	Met	Ser	Gly	Tyr	Leu	Ser	Gly	Phe	Gln	Ala	Arg	Asn	Ala	Leu	
			260					265					270			
ctt	cag	tca	aat	ctc	tct	caa	act	cag	cta	gct	act	att	tgg	act	ctg	864
Leu	Gln		Asn	Leu	Ser	Gln	Thr	Gln	Leu	Ala	Thr	Ile	Trp	Thr	Leu	
			275				280					285				
gct	gac	atc	gat	ggg	gac	gga	cag	ttg	aaa	gct	gaa	gaa	ttt	att	ctg	912
Ala	Asp	Ile	Asp	Gly	Asp	Gly	Gln	Leu	Lys	Ala	Glu	Glu	Phe	Ile	Leu	
	290					295					300					
gcg	atg	cac	ctc	act	gac	atg	gcc	aaa	gct	gga	cag	cca	cta	cca	ctg	960
Ala	Met	His	Leu	Thr	Asp	Met	Ala	Lys	Ala	Gly	Gln	Pro	Leu	Pro	Leu	
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acg	ttg	cct	ccc	gag	ctt	gtc	cct	cca	tct	ttc	aga	ggg	gga	aag	caa	1008
Thr	Leu	Pro	Pro	Glu	Leu	Val	Pro	Pro	Ser	Phe	Arg	Gly	Gly	Lys	Gln	
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gtt	gat	tct	gtt	aat	gga	act	ctg	cct	tca	tat	cag	aaa	aca	caa	gaa	1056
Val	Asp	Ser	Val	Asn	Gly	Thr	Leu	Pro	Ser	Tyr	Gln	Lys	Thr	Gln	Glu	
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gaa	gag	cct	cag	aag	aaa	ctg	cca	gtt	act	ttt	gag	gac	aaa	cgg	aaa	1104
Glu	Glu	Pro	Gln	Lys	Lys	Leu	Pro	Val	Thr	Phe	Glu	Asp	Lys	Arg	Lys	
		355					360					365				
gcc	aac	tat	gaa	cga	gga	aac	atg	gag	ctg	gag	aag	cga	cgc	caa	gtg	1152
Ala	Asn	Tyr	Glu	Arg	Gly	Asn	Met	Glu	Leu	Glu	Lys	Arg	Arg	Gln	Val	
	370					375					380					
ttg	atg	gag	cag	cag	cag	agg	gag	gct	gaa	cgc	aaa	gcc	cag	aaa	gag	1200
Leu	Met	Glu	Gln	Gln	Gln	Arg	Glu	Ala	Glu	Arg	Lys	Ala	Gln	Lys	Glu	
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aag	gaa	gag	tgg	gag	cgg	aaa	cag	aga	gaa	ctg	caa	gag	caa	gaa	tgg	1248
Lys	Glu	Glu	Trp	Glu	Arg	Lys	Gln	Arg	Glu	Leu	Gln	Glu	Gln	Glu	Trp	
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aag	aag	cag	ctg	gag	ttg	gag	aaa	cgc	ttg	gag	aaa	cag	aga	gag	ctg	1296
Lys	Lys	Gln	Leu	Glu	Leu	Glu	Lys	Arg	Leu	Glu	Lys	Gln	Arg	Glu	Leu	
			420					425					430			
gag	aga	cag	cgg	gag	gaa	gag	agg	aga	aag	gag	ata	gaa	aga	cga	gag	1344
Glu	Arg	Gln	Arg	Glu	Glu	Glu	Arg	Arg	Lys	Glu	Ile	Glu	Arg	Arg	Glu	
			435				440					445				
gca	gca	aaa	cag	gag	ctt	gag	aga	caa	cgc	cgt	tta	gaa	tgg	gaa	aga	1392
Ala	Ala	Lys	Gln	Glu	Leu	Glu	Arg	Gln	Arg	Arg	Leu	Glu	Trp	Glu	Arg	
			450			455					460					
ctc	cgt	cgg	cag	gag	ctg	ctc	agt	cag	aag	acc	agg	gaa	caa	gaa	gac	1440
Leu	Arg	Arg	Gln	Glu	Leu	Leu	Ser	Gln	Lys	Thr	Arg	Glu	Gln	Glu	Asp	
465					470					475					480	
att	gtc	agg	ctg	agc	tcc	aga	aag	aaa	agt	ctc	cac	ctg	gaa	ctg	gaa	1488

Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu	
485 490 495	
gca gtg aat gga aaa cat cag cag atc tca ggc aga cta caa gat gtc	1536
Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val	
500 505 510	
caa atc aga aag caa aca caa aag act gag cta gaa gtt ttg gat aaa	1584
Gln Ile Arg Lys Gln Thr Gln Thr Glu Leu Glu Val Leu Asp Lys	
515 520 525	
cag tgt gac ctg gaa att atg gaa atc aaa caa ctt caa caa gag ctt	1632
Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu	
530 535 540	
aag gaa tat caa aat aag ctt atc tat ctg gtc cct gag aag cag cta	1680
Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu	
545 550 555 560	
tta aac gaa aga att aaa aac atg cag ctc agt aac aca cct gat tca	1728
Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser	
565 570 575	
ggg atc agt tta ctt cat aaa aag tca tca gaa aag gaa gaa tta tgc	1776
Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys	
580 585 590	
caa aga ctt aaa gaa caa tta gat gct ctt gaa aaa gaa act gca tct	1824
Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser	
595 600 605	
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Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg	
610 615 620	
gaa agc tat aat aca cag cag tta gcc ctt gaa caa ctt cat aaa atc	1920
Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile	
625 630 635 640	
aaa cgt gac aaa ttg aag gaa atc gaa aga aaa aga tta gag caa att	1968
Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile	
645 650 655	
caa aaa aag aaa cta gaa gat gag gct gca agg aaa gca aag caa gga	2016
Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly	
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aaa gaa aac ttg tgg aga gaa agt att aga aag gaa gaa gag gaa aag	2064
Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Glu Lys	
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caa aaa cga ctc cag gaa gaa aag tca cag gac aaa act caa gaa gag	2112
Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu	
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Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val	
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aat tac aga gca ctg tac cct ttt gaa gca aga aac cat gat gag atg	2208

Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met	
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Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly	
740 745 750	
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Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe	
755 760 765	
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Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser	
770 775 780	
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Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser	
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Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe	
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acc cgc act gtg tcc cct gga tct gtg tcc ccc att cac gga cag ggg	2544
Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly	
835 840 845	
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Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala	
850 855 860	
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Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val	
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Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg	
885 890 895	
gga tgg ttc ccc aag tct tat gtc aag ctc att cct ggg aat gaa gta	2736
Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val	
900 905 910	
cag cga gga gag cca gaa gct ttg tat gca gct gtg act aag aaa cct	2784
Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro	
915 920 925	
acc tcc aca gcc tat cca gtt acc tcc aca gcc tat cca gtt gga gaa	2832
Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu	
930 935 940	
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Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu	
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act ttc act gaa ggt gaa gaa att cta gtg acc cag aaa gat gga gag	2928

Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu	
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Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn	
980 985 990	
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Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser	
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Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr	
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Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln	
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gcc aga ggg aag aaa cga cag aag gga tgg ttt cct gcc agc cat gta	3216
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Glu Leu Asn Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys Asp	
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Asp Pro Asp Trp Trp Gln Gly Glu Thr Asn Gly Leu Thr Gly Leu Phe	
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cct tca aac tat gtt aag atg aca aca gac tca gat cca agt caa cag	3456
Pro Ser Asn Tyr Val Lys Met Thr Thr Asp Ser Asp Pro Ser Gln Gln	
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Trp Cys Ala Asp Leu Gln Ala Leu Asp Thr Met Gln Pro Thr Glu Arg	
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Lys Arg Gln Gly Tyr Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr	
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Met Asp Asp Asp Leu Gln Leu Val Ile Glu Val Phe Gln Lys Arg Met	
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Ala Glu Glu Gly Phe Leu Thr Glu Ala Asp Met Ala Leu Ile Phe Val	
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Asn Trp Lys Glu Leu Ile Met Ser Asn Thr Lys Leu Leu Arg Ala Leu	
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cgg gtg agg aag aag act ggg ggt gag aag atg cca gtt cag atg att	3744
Arg Val Arg Lys Lys Thr Gly Gly Glu Lys Met Pro Val Gln Met Ile	
1235 1240 1245	
gga gac atc ctg gcg gca gag ctg tcc cac atg cag gcc tac atc cgc	3792
Gly Asp Ile Leu Ala Ala Glu Leu Ser His Met Gln Ala Tyr Ile Arg	
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Phe Cys Ser Cys Gln Leu Asn Gly Ala Thr Leu Leu Gln Gln Lys Thr	
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gac gag gac acg gac ttc aag gaa ttt cta aag aag ttg gca tca gac	3888
Asp Glu Asp Thr Asp Phe Lys Glu Phe Leu Lys Lys Leu Ala Ser Asp	
1285 1290 1295	
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Pro Arg Cys Lys Gly Met Pro Leu Ser Ser Phe Leu Leu Lys Pro Met	
1300 1305 1310	
cag agg atc act cgc tac ccg ctg ctc atc cga agt atc ctg gag aac	3984
Gln Arg Ile Thr Arg Tyr Pro Leu Leu Ile Arg Ser Ile Leu Glu Asn	
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Thr Pro Gln Ser His Val Asp His Ser Ser Leu Lys Leu Ala Leu Glu	
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Gly Leu Ala Glu Gln Leu Ile Phe Asn Ser Leu Thr Asn Cys Leu Gly	
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ccc cgg aag ctt ctg cac agc ggg aag ctg tac aag acc aag agc aat	4224
Pro Arg Lys Leu Leu His Ser Gly Lys Leu Tyr Lys Thr Lys Ser Asn	
1395 1400 1405	
aag gag ctg cac gcc ttc ctc ttc aac gac ttc ctg ctg ctc acc tac	4272
Lys Glu Leu His Ala Phe Leu Phe Asn Asp Phe Leu Leu Leu Thr Tyr	
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Leu Val Arg Gln Phe Ala Ala Ser Gly His Glu Lys Leu Phe Asn	
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Ser Lys Ser Ser Ala Gln Phe Arg Met Tyr Lys Thr Pro Ile Phe Leu	
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Val Phe His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Thr Asp	
1475 1480 1485	
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Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser Tyr Thr Thr Arg Thr	
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1570 1575 1580	
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Ile Lys Asp Leu Tyr Gln Asp Val Leu Cys Leu Thr Met Phe Asp Arg	
1585 1590 1595 1600	
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Asp Gln Phe Ser Pro Asp Asp Phe Leu Gly Arg Thr Glu Val Pro Val	
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Ala Lys Ile Arg Thr Glu Gln Glu Ser Lys Gly Pro Thr Thr Arg Arg	
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 Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe  
 35 40 45  
 Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu  
 50 55 60  
 Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile  
 65 70 75 80  
 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val  
 85 90 95  
 Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile  
 100 105 110  
 Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln  
 115 120 125  
 Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr  
 130 135 140  
 Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro  
 145 150 155 160  
 Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln  
 165 170 175  
 Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser  
 180 185 190  
 Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala  
 195 200 205  
 Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala  
 210 215 220  
 Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val  
 225 230 235 240  
 Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp  
 245 250 255  
 Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu  
 260 265 270  
 Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu  
 275 280 285  
 Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu  
 290 295 300  
 Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu

305		310		315		320
Thr Leu Pro Pro	Glu Leu Val Pro Pro	Ser Phe Arg Gly Gly	Lys Gln			
	325	330	335			
Val Asp Ser Val	Asn Gly Thr Leu Pro	Ser Tyr Gln Lys Thr	Gln Glu			
	340	345	350			
Glu Glu Pro Gln	Lys Lys Leu Pro Val Thr	Phe Glu Asp Lys Arg	Lys			
	355	360	365			
Ala Asn Tyr Glu	Arg Gly Asn Met Glu Leu Glu	Lys Arg Arg Gln	Val			
	370	375	380			
Leu Met Glu Gln	Gln Gln Arg Glu Ala Glu Arg	Lys Ala Gln Lys	Glu			
	385	390	395	400		
Lys Glu Glu Trp	Glu Arg Lys Gln Arg Glu Leu	Gln Glu Gln Glu	Trp			
	405	410	415			
Lys Lys Gln Leu	Glu Leu Glu Lys Arg Leu Glu	Lys Gln Arg Glu	Leu			
	420	425	430			
Glu Arg Gln Arg	Glu Glu Glu Arg Arg Lys Glu	Ile Glu Arg Arg	Glu			
	435	440	445			
Ala Ala Lys Gln	Glu Leu Glu Arg Gln Arg Arg	Leu Glu Trp Glu	Arg			
	450	455	460			
Leu Arg Arg Gln	Glu Leu Leu Ser Gln Lys Thr Arg	Glu Gln Glu Asp				
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Ala Val Asn Gly	Lys His Gln Gln Ile Ser Gly Arg	Leu Gln Asp Val				
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Gln Ile Arg Lys	Gln Thr Gln Lys Thr Glu Leu Glu	Val Leu Asp Lys				
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Gln Cys Asp Leu	Glu Ile Met Glu Ile Lys Gln Leu Gln	Gln Glu Leu				
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Lys Glu Tyr Gln	Asn Lys Leu Ile Tyr Leu Val Pro	Glu Lys Gln Leu				
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Leu Asn Glu Arg	Ile Lys Asn Met Gln Leu Ser Asn Thr	Pro Asp Ser				
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Gly Ile Ser Leu	Leu His Lys Lys Ser Ser Glu Lys	Glu Glu Leu Cys				
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Gln Arg Leu Lys	Glu Gln Leu Asp Ala Leu Glu Lys	Glu Thr Ala Ser				
	595	600	605			
Lys Leu Ser Glu	Met Asp Ser Phe Asn Asn Gln Leu	Lys Glu Leu Arg				
	610	615	620			
Glu Ser Tyr Asn	Thr Gln Gln Leu Ala Leu Glu Gln	Leu His Lys Ile				



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Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile	645	650	655
Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly	660	665	670
Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Lys	675	680	685
Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu	690	695	700
Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val	705	710	715
Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met	725	730	735
Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly	740	745	750
Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe	755	760	765
Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser	770	775	780
Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser	785	790	795
Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser	805	810	815
Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe	820	825	830
Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly	835	840	845
Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala	850	855	860
Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val	865	870	875
Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg	885	890	895
Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val	900	905	910
Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro	915	920	925
Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu	930	935	940
Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu			

945		950		955		960
Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu						
	965			970		975
Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn						
	980		985		990	
Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser						
	995	1000		1005		
Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr						
1010		1015		1020		
Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile						
025	1030		1035		1040	
Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln						
	1045		1050		1055	
Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro Ala Ser His Val						
	1060		1065		1070	
Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met Pro Thr Phe His Ala						
1075		1080		1085		
Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Met Ala Asn Asn Glu Asp						
1090		1095		1100		
Glu Leu Asn Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys Asp						
105	1110		1115		1120	
Asp Pro Asp Trp Trp Gln Gly Glu Thr Asn Gly Leu Thr Gly Leu Phe						
	1125		1130		1135	
Pro Ser Asn Tyr Val Lys Met Thr Thr Asp Ser Asp Pro Ser Gln Gln						
	1140		1145		1150	
Trp Cys Ala Asp Leu Gln Ala Leu Asp Thr Met Gln Pro Thr Glu Arg						
1155		1160		1165		
Lys Arg Gln Gly Tyr Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr						
1170		1175		1180		
Met Asp Asp Asp Leu Gln Leu Val Ile Glu Val Phe Gln Lys Arg Met						
185	1190		1195		1200	
Ala Glu Glu Gly Phe Leu Thr Glu Ala Asp Met Ala Leu Ile Phe Val						
	1205		1210		1215	
Asn Trp Lys Glu Leu Ile Met Ser Asn Thr Lys Leu Leu Arg Ala Leu						
	1220		1225		1230	
Arg Val Arg Lys Lys Thr Gly Gly Glu Lys Met Pro Val Gln Met Ile						
	1235		1240		1245	
Gly Asp Ile Leu Ala Ala Glu Leu Ser His Met Gln Ala Tyr Ile Arg						
1250		1255		1260		
Phe Cys Ser Cys Gln Leu Asn Gly Ala Thr Leu Leu Gln Gln Lys Thr						

265	1270	1275	1280
Asp Glu Asp Thr Asp Phe Lys Glu Phe Leu Lys Lys Leu Ala Ser Asp	1285	1290	1295
Pro Arg Cys Lys Gly Met Pro Leu Ser Ser Phe Leu Leu Lys Pro Met	1300	1305	1310
Gln Arg Ile Thr Arg Tyr Pro Leu Leu Ile Arg Ser Ile Leu Glu Asn	1315	1320	1325
Thr Pro Gln Ser His Val Asp His Ser Ser Leu Lys Leu Ala Leu Glu	1330	1335	1340
Arg Ala Glu Glu Leu Cys Ser Gln Val Asn Glu Gly Val Arg Glu Lys	345	1350	1355
Glu Asn Ser Asp Arg Leu Glu Trp Ile Gln Ala His Val Gln Cys Glu	1365	1370	1375
Gly Leu Ala Glu Gln Leu Ile Phe Asn Ser Leu Thr Asn Cys Leu Gly	1380	1385	1390
Pro Arg Lys Leu Leu His Ser Gly Lys Leu Tyr Lys Thr Lys Ser Asn	1395	1400	1405
Lys Glu Leu His Ala Phe Leu Phe Asn Asp Phe Leu Leu Leu Thr Tyr	1410	1415	1420
Leu Val Arg Gln Phe Ala Ala Ala Ser Gly His Glu Lys Leu Phe Asn	425	1430	1435
Ser Lys Ser Ser Ala Gln Phe Arg Met Tyr Lys Thr Pro Ile Phe Leu	1445	1450	1455
Asn Glu Val Leu Val Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro	1460	1465	1470
Val Phe His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Thr Asp	1475	1480	1485
Asn Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Gly Ala Ser	1490	1495	1500
Glu Gln Tyr Ile Asp Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr Gln	505	1510	1515
Ala Arg Ser Gln Lys Thr Ser Gly Ile Gly Arg Leu Met Val His Val	1525	1530	1535
Ile Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn Gly Lys Ser Asn	1540	1545	1550
Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser Tyr Thr Thr Arg Thr	1555	1560	1565
Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn Phe Asn Cys Gln Phe Phe	1570	1575	1580
Ile Lys Asp Leu Tyr Gln Asp Val Leu Cys Leu Thr Met Phe Asp Arg			

[illegible]

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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<211> 21

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:peptide

<400> 33

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Ile Thr Val Glu Glu  
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